



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/675,470

Source:

1-7-016

Date Processed by STIC:

1-4-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/675,470

DATE: 01/04/2005
TIME: 10:02:47

Input Set : A:\SEQUENCE LISTING.asc
Output Set: N:\CRF4\01042005\J675470.raw

SEQUENCE LISTING

2 (1) GENERAL INFORMATION:
3 (iii) NUMBER OF SEQUENCES: 4
C--> 0 (vi) CURRENT APPLICATION DATA:
C--> 0 (A) APPLICATION NUMBER: US/10/675,470
C--> 0 (B) FILING DATE: 30-Sep-2003

ERRORED SEQUENCES

5 (2) INFORMATION FOR SEQ ID NO: 1:
6 (i) SEQUENCE CHARACTERISTICS:
7 (A) LENGTH: 4 amino acids
8 (B) TYPE: amino acid
9 (C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear
11 (ii) MOLECULE TYPE: peptide
12 (iii) HYPOTHETICAL: NO
13 (iv) ANTI-SENSE: NO
14 (v) FRAGMENT TYPE: N-terminal
15 (vi) ORIGINAL SOURCE:
16 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

E--> 17 ~~Norleucine-Tyr-Ile-His~~

19 (2) INFORMATION FOR SEQ ID NO: 2:
20 (i) SEQUENCE CHARACTERISTICS:
21 (A) LENGTH: 4 amino acids
22 (B) TYPE: amino acid
23 (C) STRANDEDNESS: single
24 (D) TOPOLOGY: linear
25 (ii) MOLECULE TYPE: peptide
26 (iii) HYPOTHETICAL: NO
27 (iv) ANTI-SENSE: NO
28 (v) FRAGMENT TYPE: N-terminal
29 (vi) ORIGINAL SOURCE:
30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

E--> 31 ~~Norleucine-Tyr-Ile-(6-Aminohexanoic Acid)-amide~~

34 (2) INFORMATION FOR SEQ ID NO: 3:
35 (i) SEQUENCE CHARACTERISTICS:
36 (A) LENGTH: 6 amino acids
37 (B) TYPE: amino acid
38 (C) STRANDEDNESS: single
39 (D) TOPOLOGY: linear
40 (ii) MOLECULE TYPE: peptide

Does Not Comply
Corrected Diskette Needed

Amino Acid (pg. 1-2) ←

pls use (3) letter
base codes.

delete

pls use (3) letter
Amino acid base codes.

delete

RAW SEQUENCE LISTING

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Input Set : A:\SEQUENCE LISTING.asc

Output Set: N:\CRF4\01042005\J675470.raw

41 (A) DESCRIPTION: Norleucine(1)- Angiotensin IV
 42 (iii) HYPOTHETICAL: NO
 43 (iv) ANTI-SENSE: NO
 44 (v) FRAGMENT TYPE: N-terminal
 C--> 45 (vi) ORIGINAL SOURCE:
 46 (ix) FEATURE:

47 (A) NAME/KEY: Modified-site
 48 (B) LOCATION: N-terminal amino acid
 49 (D) OTHER INFORMATION:
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

E--> 51 ~~Norleucine-Tyr-Ile-His-Pro-Phe~~

54 (2) INFORMATION FOR SEQ ID NO: 4:

55 (i) SEQUENCE CHARACTERISTICS:
 56 (A) LENGTH: 6 amino acids
 57 (B) TYPE: amino acid
 58 (C) STRANDEDNESS: single
 59 (D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide
 61 (A) DESCRIPTION: Norleual

62 (iii) HYPOTHETICAL: NO
 63 (iv) ANTI-SENSE: NO
 64 (v) FRAGMENT TYPE: N-terminal
 65 (vi) ORIGINAL SOURCE:
 66 (ix) FEATURE:

67 (A) NAME/KEY: Modified-site
 68 (B) LOCATION: Multiple
 69 (D) OTHER INFORMATION:

70 /note= Leu3-His4 is a methylene bond
 71 instead of a peptide bond.

72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

E--> 73 ~~Norleucine-Tyr-Leu-His-Pro-Phe~~

pls use (3) letter base codes.

pls refer to 1.822 old Sequence Rules Format

pls use (3) letter base codes.

Same error

↑ FYI: Amino acid sequence should be grouped as:
 Tyr Leu His Pro

↑ pls use (3) letter

VERIFICATION SUMMARY

DATE: 01/04/2005

PATENT APPLICATION: US/10/675,470

TIME: 10:02:48

Input Set : A:\SEQUENCE LISTING.asc

Output Set: N:\CRF4\01042005\J675470.raw

L:0 M:200 E: Mandatory Header Field missing, [(i) APPLICANT:] of (1)
 L:0 M:200 E: Mandatory Header Field missing, [(ii) TITLE OF INVENTION:] of (1)
 L:0 M:200 E: Mandatory Header Field missing, [(A) ADDRESSEE:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(B) STREET:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(C) CITY:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(D) STATE:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(E) COUNTRY:] of (1)(iv)
 L:0 M:200 E: Mandatory Header Field missing, [(F) ZIP:] of (1)(iv)
 L:0 M:249 C: Inserted Mandatory Field, [(vi) CURRENT APPLICATION DATA:]
 L:0 M:249 C: Inserted Mandatory Field, [(A) APPLICATION NUMBER:]
 L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
 L:17 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:17 M:330 E: (2) Invalid Amino Acid Designator, 1
 L:17 M:203 E: No. of Seq. differs, LENGTH:Input:4 Found:1 SEQ:1
 L:31 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:31 M:330 E: (2) Invalid Amino Acid Designator, 2
 L:31 M:203 E: No. of Seq. differs, LENGTH:Input:4 Found:2 SEQ:2
 L:45 M:220 C: Keyword misspelled or invalid format, [(vi) ORIGINAL SOURCE:]
 L:51 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:51 M:330 E: (2) Invalid Amino Acid Designator, 1
 L:51 M:203 E: No. of Seq. differs, LENGTH:Input:6 Found:1 SEQ:3
 L:73 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:73 M:330 E: (2) Invalid Amino Acid Designator, 1
 L:73 M:203 E: No. of Seq. differs, LENGTH:Input:6 Found:1 SEQ:4